

Serial No. 10/786,679
Amendment Dated December 20, 2006
Reply to Office Action of September 26, 2006

APPENDIX

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 7071378_SEQ_1 check: 9103 from: 1 to: 531

WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 162 Length: 39
Ratio: 4.154 Gaps: 0

Percent Similarity: 69.231 Percent Identity: 69.231

Match display thresholds for the alignment(s):

| = IDENTITY

:= 5

$$\cdot = 1$$

1587 SEQ 1 x 7071378 SEQ 1 December 15, 2006 16:23 ..

199 tttactaaaat~~tttctgtat~~agtaacatgtcataact 237
||||| ||||| | |||| | ||| ||| ||| ||| ||| |
355 tt~~tat~~aaaact~~qtctt~~aaaata~~qqqc~~caactcataat 393

Input Sequence: 1587 SEQ 1

```
!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ...
1  gaattcggccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgcgg
101  atataaaaaaa aaaacgccag tcatttatgg tacgggattta ataggttcca
151  agaaccagcc acaatccatt tatttagttc atataaatgt cataaatttt
201  tactaaaatt ttctctgtat agtaacatgt cataactgaa ctttgtgagaa
251  aaacgccagt tatttatggc acgggattaa taggttccaa aaaccagccg
301  taaccttattt atatttagggc actttaagct ggtgcctca gttttgttgg
```

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351 tgtcttcgtt tttaaactta gttgtatttt ttttcttagt tctgtccttc
401 tagtgttata gagcataagg aaaaaattga gaaaaaaatg actaaggata
451 aaaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 7071378_SEQ_1

!!NA_SEQUENCE 1.0
WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4
7071378_SEQ_1 Length: 531 December 15, 2006 16:20 Type: N Check: 9103
..
1 gatcattaag gactaaggcag tcttttccc tttcggcttg catcatctt
51 agtcttcatc actattataa gccgaagcta ttaccccttg gctatagctt
101 cgggtttcat cttttattatc ttccggactat gtcttcaccc tttataccctt
151 tgtcttgggg gaaaaccccttc atcctgaagc cgaagctccc tgtaataatt
201 catatcatgc taaaaataaa tggtcagtcc ttgttttgag gacccctcgga
251 agaggaaggc cccccaacaa gacgattaac tagtattgtc tcactgcatt
301 gttttttgg cacttcatca ataatgcctc aatagcatac ttcatatcc
351 gaactttatt aaaaactgtct taaaataggg ccaagtcata aattcattca
401 aagtgactct tcatttctta cttcctatct ttgggtggttt tgtatataata
451 tatgttcatg gttgagtgat gttcctacac cactacacca cacgttagat
501 atatatacag aaaaatagctt cactatctag a

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 7071378_SEQ_2 check: 806 from: 1 to: 2493

WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 139 Length: 31
Ratio: 4.484 Gaps: 0
Percent Similarity: 70.968 Percent Identity: 70.968

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 7071378_SEQ_2 December 15, 2006 15:59 ..

526 agtatactccaaggcacattgaatttggatt 556
| | || |||| ||||| |||||||| ||
525 attttagaccaaaccattnaaatttggttt 555

Input Sequence: 1587_SEQ_1

!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

1 gaattcggccc ttggtagatg tcttagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggc acgggattaa taggttccaa aaaccagccg
301 taaccttattt atattagggt actttaagct ggtgcctca gttttgttgg
351 tgtcttcgtt tttaaactta gttgtatTTT ttttcttagt tctgtccttc

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401 tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 7071378_SEQ_2

!!NA_SEQUENCE 1.0
WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986
7071378_SEQ_2 Length: 2493 December 15, 2006 15:57 Type: N Check: 806
..

1 aagctttcc ggtgatgaag cacctgtaat acttaacagc atgctgaaaa
51 caaatagttt gctgtgttt tgaggacctt cggaagatga aggcccccaa
101 cacatcccat gcatcaagtc cccatgactt gcaaaaaagc aaattttatc
151 aaaatttctc ataaaaacact tggaaacatt tctcttttg aaaagtgtag
201 agcactagca actgtctact aaaaaggttc ccaaatttct gggtataaca
251 atcgcatggt aaataacaca aaggaaatcc tactaagagc agtaatttgg
301 ctaaaacaat agtgaggatt ttaatgtaat aggaaatagg agcatgcaat
351 acttgtgttc tttcagggtt ttgatgtcct caaaagtgtg cccccctggg
401 gcagttgcaa cactcaaaat ctactcgtat acataaagaa acatgggcac
451 aaaataagaa acaataactca aattatgaaa aaggttcaaa tggcctata
501 attattgttag acattttaga atttattttt gaccaaaacc atttaaattt
551 ggtttaaaat gagttagata ttaatattta ttcagtttat agttatttgg
601 gacattttt tacttaacta taacttctag ggtttaaaa gtaaattttg
651 ggtccctagt tggaaactagc tcagattgct ggttgatttc cataaaagtc
701 gaggttcctt tagcaaaaat ccacggtgaa caagggggag ataggtgttg
751 accgatatct ctaaattttg atcggtggac ggcacatgga tgtctcagat

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801 taaatggtgg atgtgcaagc gacgcgcaca cgatggagga atggcttcac
851 gacggtgggc tactagagct ggctacgtca accaatggag ggctcggtca
901 aggtcaaaaat ttgttccaa gccactgtgg ctcacatga gtcgatttag
951 cacatataaa ggtcgagggt caaccagagg ggcaagatcg atggtgca
1001 ggtgttctcg atggaagggg aaacttcggg gagcaattca agatttccta
1051 tcatgtgacc gggtcaggga atggcgcat ggggtttggg accttctgg
1101 gcacatcatg ttgctgtatc gatgtcaagg gagcattagg gttcacgagt
1151 cagcgatgac gggcatggg gggacttgggt caccatgggt cgatcaacta
1201 gggacgatag agctctatga agttcacaa cttcctcaca ctctagggat
1251 catggtgaca aaggtgggg ggcacggggcg tctctagtga gggtgaaatg
1301 cagttctgtc acgtggaaat agtggcggca tcgcttgtaa tgaataaaag
1351 gtgcttgggt ggctgggaag tgcaatatga gggaaagttagt tggtgccggg
1401 atgttccttt tataagggag caccattgtat taatgaaaga caatgacaca
1451 aagggtgggt cgacagttt aagctcgaat gctgctaggg gtgctcaagg
1501 taaaagatc aggcattcagg gaggaaaggc agggataaaa tttcttact
1551 ccagttgtgg ggtgatgggg acaagggttag tgctcaagca agggagggcg
1601 agttcagcgc agagatgcct gttgtgacac atgggggggg gggatttgg
1651 ggttgggggtt gaccaggtaa cggtatggcg tgaccaggag aagagaccca
1701 ctgatgggg aaaaaggtaa caacaggtaa ggaccaagggt gtcagtgact
1751 caccgtgaca tggatgggaa aagttacgtc cgaaatgggt tgggcctgag
1801 tggatgttgc tggctcgggc actgtgctga tccttaatt tctccattcc
1851 caatttaagt tgaatttttta attcaaataa aatgactcca aatctctcca
1901 aaattacaa aatataaaat atttagatga atatgttggg ggagtttggg
1951 ctccgctttt ggttagtatg tttgtataaa aataatttct ctcctttgt
2001 cacttccaaat attgacttaa atttttatgt agcaatgcca actttttta
2051 gtagtgtgcc acttatacgca caaaaactat atccatttc taatagtc
2101 tggaaatccac attctatggg tagccattct tcaaaaattgg cacaacta

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2151 ggaaaattta atacattctt gccataacat attctagtgc aatgttaac
2201 tagattgctc aatattagca aacttctttt gtaagattca ttaatattgc
2251 tacattgcat acttttttag aagttcatca ataatgcctc attagcatac
2301 ttcatttttag gaacttgatt aaaaccgcct taaaatagag ccaagtgacg
2351 gatccattta aaggtgattc ttaatttctt acttcctatc tttggtggt
2401 tatgtttata tatgtgtggg tggttgaatg atgttcctac accactacac
2451 cacacgttgg acatatatat gaaaaatagc ttcacagtct aga

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590
to: 7071378_SEQ_3 check: 9984 from: 1 to: 1708
WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at position 1193

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000
Quality: 165 Length: 45
Ratio: 3.667 Gaps: 0
Percent Similarity: 66.667 Percent Identity: 66.667

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 7071378_SEQ_3 December 15, 2006 16:24 ..

199 tttactaaaatttctctgtatagtaacatgtcataactgaactt 243
||||| ||||||| |||| ||||| ||| ||| ||| |||
1529 ttatgaaaattgtctaaaatagggccaagtcacaaatccactt 1573

Input Sequence: 1587_SEQ_1

!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..
1 gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggc acgggattaa taggttccaa aaaccagccg
301 taaccttattt atattagggt actttaagct ggtgcctca gttttgttgg
351 tgtcttcgtt tttaaactta gttgtatTT ttttcttagt tctgtccttc

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401 tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 7071378_SEQ_3

!!NA_SEQUENCE 1.0
WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at
position 1193
7071378_SEQ_3 Length: 1708 December 15, 2006 16:22 Type: N Check: 9984
..
1 aagcttagaa atttaaaaa aagccaggca agcgttggtg tgcaaagagc
51 taaaaattag gaagacaaga gaacacggca agaaagcatg ctaaatgtgc
101 tcgcggtgcg ttcttattta tacgctcaat acgttgcaag tggtagggcc
151 ccacttgtca ttgactattg ctattcttagc aaagggaagg tgttttcgg
201 accttcggct taaggccttc gtccatatcg caatctgaat ttatcattct
251 aacaaattaa tattgtgagg ggctactgtt gggggccttc gacttccgaa
301 ggtcctcaaa aactggttt aacgtgttcc tggagtataa tgcataaaaca
351 ggtatctcg ggtttggatc agaactacaa catgaagagg cacaaagaaac
401 acgaaggttg ggcgcagagcc gaagctcacg tgttaggagag cttcggcacg
451 acagcagaaa aagggaaccg actttaaagg aaaggctatt cagacctcga
501 tggatttcta taggtcatta gcaaatgtaa agggcatgaa tgtaattttta
551 catgggctgt gtccttgccataaaatagat gaacagtact ctcgtactgt
601 tcacgctgac ttggcattcg cttttgcat cacgcttgcata cccttgcttt
651 ccttcaaacc gaaggtacat ctataatttgc ttattgtgtt attgtggata
701 tggtaatgca aataaaaata agttgatgat aatgtttata ttatTTTcg

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751 tatttcatat atgaattctt cctcatcatt tatttgctt acgaaggttt
801 ttccttcaaa atctttgtcc ggaattcatt atatccgaag ggaaataatg
851 tctcgaagga cgaaggactt tgatatttaa cactttcat gttgccttgt
901 tcttgactct tagcattga gaacaagtcc ccaacagctc ctaagctctt
951 ctttgaagaa acaactacta gatgaagttt ctccaaaagt acgtccattg
1001 aatggagtaa agagtcattt gacctctcg aataaaatta aatgagaat
1051 aagtaagaat aaaacacctc tattatcaaa tctaggccat acaaacattg
1101 ggtattacta aaaaatagct aatgccatct ttcaacattt ggaagttaaa
1151 accaaccaat cctcactcat tcccaagaaa tattggatca tatttaacat
1201 tttgtgtcac ttacaaaaat ggcttaatct tttatgcggc aatgccaacc
1251 ttttttagca gggtgccact tgtaacatga aaactataac tattttcaaa
1301 tagtaccttg aaattcgcatt tctatttta tgcattcttc aaaattgaca
1351 caaattaaac taggagaatt caatacattc ttgccataac atattctaatt
1401 gcaaataattt agtagattgc tcaacatcggt tacacatctt ttggacgatt
1451 aatttagtatt gtctcaactac attctttgtt ttagcagttc atcaataatg
1501 cctcaatagc atacttcatt ttaggaactt tatgaaaatt gtcttaaaat
1551 agggccaagt cacaaatcca ctcaaagggt gactcttcat ttcttacttc
1601 ctatcttgc ttgttttgtt atatatatgt gtggatggtt gagtgatgtt
1651 cctacaccac tacaccacac cttagacaca tatatggaaa atagcttcac
1701 tgcttaga

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_1 check: 2029 from: 1 to: 4305

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 169 Length: 67
Ratio: 2.770 Gaps: 2
Percent Similarity: 72.131 Percent Identity: 72.131

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 6777591_SEQ_1 December 15, 2006 17:07 ..

161 acaatccatatttagttcatataaatgtcata....aattttta..ct 204
||||||| || | || | | ||| ||| | ||| | ||| ||| ||| ||| ||| |||
956 acaatcaaatatgataatataataataataattcaattttaatct 1005

205 aaaattttctctgtata 221
| | | | | | | |||||
1006 acaatttttaattata 1022

Input Sequence: 1587_SEQ_1

!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

1 gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg

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351 tgtcttcgtt tttaaactta gttgtatttt ttttcttagt tctgtccttc
401 tagtgttata gagcataagg aaaaaattga gaaaaaatg actaaggata
451 aaaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 6777591_SEQ_1

!NA_SEQUENCE 1.0
6777591_SEQ_1 Length: 4305 December 15, 2006 17:05 Type: N Check: 2029
..
1 ttcaaaaccc gattcccgag gcggccctat tgaagatatg ggggaagttc
51 gacgagatcg atgtcgggtc gagtgctatg gtgtatggc cgtttgggg
101 gaggatgagc gagatagcca agactagcat tccgttccca cacagagttg
151 ggaatttgta ccaaattccaa cacttgcgtt attggagcga cgatagggac
201 gcggaaaaac acatccgtt gatcagggag ttgtacgtt atctcgagcc
251 ttatgtgtcg aagaatccga ggtatgctta cgtgaactac agggatctcg
301 acatcggat gaatggagga ggtgaagggg atgagaaggg tacttatggt
351 gaggctaagg tgtggggga gaagtacttt ggggtcaact ttgtatcggtt
401 gggtcggtg aagacgattt ttgtatccaa taatgtgtt cggaaacgagc
451 agagcattcc ctcaattcca actcggttat aaggatcaat gatcaatgag
501 aatttccctt tccaaatgtga ttacaagttc tattgggtca gctttctcaa
551 ctgctcctat tcatttagat taattcataa caactattaa ttaccagcc
601 ttttatccgg cccgttggcc gatttatttt cttaagttt agatgaaatg
651 aaaccgattt agtttttatt gagatgagat taatcttaat ttgcttgaaa
701 ttactcacg gttgtatgtga tatttggaaat taactaaaat gataaatatc

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751 ggataaaaat aaaaatattt aaaataaata acataaacat aagaacaata
801 aaataaataa atttaatttt aatttatttc cttgtttct ttctgtatca
851 tacatctctt ctcttacttc ttaaaggctt ttcaattatc acttaattaa
901 atacaataga taaatcgta attctataac attaacctat acacttgac
951 ggtgaacaat caatatgata atataataat aatataataa ttcaattatt
1001 aatctacaat ttttaatta taaagtttat gcggtcagtt tctgcaagct
1051 ccgagctcct tgtcatcggt agtttctgcg gtctcaaggt ataacgactc
1101 ggagcgacga gcccttgct tccaatggac gggttgcatt tctgccgtcg
1151 ttgagctcga ttggcgtgtc atgctggagt cagagttcct aaaaaaaaaac
1201 cctaaactag agggtgatta gggtaaaatt agggtgttgg cctgggttcc
1251 attgtccaaa gtttagtca actaaaaac agacttaat tttatgcttc
1301 aaaatagttt atctgttatt atattagcgt gtaattagtc ttgacaatgg
1351 ggccggacgg gtacggattc gggaccccgaa tcccccccc tagtgtaatg
1401 gctcaactgc caagtcaagca ttggaccgaa attattggac acgaagttact
1451 aatgtgaaaa actttacatt tggatatttc tacttaata ctatgctatt
1501 ttcaaaattt gaacttaat actatgttt tatatagttt agtataatctt
1551 aattttatg caaatttcattc taattgtatt aaactatTTT cgatccgttag
1601 ctaatttattt cgaaggcaag tcaaagtgtt attgtggact atgtgagctt
1651 atattgaacc tttatctctc ccaaccactc aagttaattt aacccaaactc
1701 gatcggttgg gtttcgagct atttcgagcc attgtgttta tatgcacgtg
1751 agatatacaag attgaccgaa acactttattt atgataatgt agaaaaagaa
1801 aacatattct aagactacat gcatgcaaag tgcaacccct gcatggaaag
1851 ctgctcaaca cgtggcatag actcccgcca cgtgtccatt ccacccatc
1901 acctcaccccc caccgttcac ctcttattat atcacaacaa tcaatcaatc
1951 ctactcctcc atactcgaac aaatccgacc aacttataacc aatattccca
2001 aacttgatta atttctcagc aatatggatc agacgcacca gacatacgcc
2051 ggaaccacgc agaaccgag ctatggcggc gggggcacaa tgtaccagca

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2101 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg
2151 cgggtggatc cctcatcggtt ctgtccggtc tcatccttac ggccaccgtc
2201 atttcactca tcatagccac ccctctcctt gtcatcttca gccctgttct
2251 tgtcccggtct ctcatcaccg tcgggctctt gatcaccggg tttcttgctt
2301 ccgggtgggtt cggagtcgcc gccgtcaccg tcttgcctg gatctatagg
2351 tatgtataag ctttggactt tagtattgtt ataaaataca taagctgatt
2401 tatgaacatg gatctccaa caagagttat ttaaatgcat tctcggtctg
2451 actcgatcg ttgggtttt agctactcg tcacaatggt cgggtcggt
2501 ctggatctgt tatactaata ttggaaagcc tgaagttca ttgttctgcc
2551 ccaacttccc actacctttt gagggtgtta agaaggccata caaactaatt
2601 atgaatccct cccaacaact cagaactcga gtcagtggt tgcgtacgggt
2651 ctctataaac attcgaaaaa tctttgttca atgaacgtag aaatgaccat
2701 gcttgatgat tgtgggtctt ataaggtagtgc tgaccggcgg gcacccggcgg
2751 ggaggggatt cgctggacca ggcttaggtcg aagctggccg gaaaggccag
2801 ggaggtgaag gacagggcgt cggagttcgc acagcagcat gtcacaggtg
2851 gtcaacagac ctcttaaaga gagtcctcta gttaaattgg tcttcgtttc
2901 tgtttcgtgg cggcttgtaa actcttttt aagtgtgctg ttttcctttt
2951 gtctcgtgtg ttgttaagtga aagtgtatc gaagtccaa gttggagatg
3001 ttgttaacga tgatgtttc taataatcag agatattaaa agggttgcta
3051 atttagtatt gcgtctgatc tcggaccaaa ctcgcaagta aaattgcaga
3101 ggatgagttg tacagaacaa gcgtgcattt ttctgaaagt tcatttcctt
3151 ggagccgacc ttgttgctt cagttcgcc aagtccacta gacaatgttta
3201 cgagttaagc ctctgtcaaa cagatcgctc tagcgtccca gaaaacacca
3251 gattttcga aaaccatcggtt ggttcaattt tcgattcaat tccgatcttgc
3301 gaagtacttg aacagaagca tgatgctaaa agataataga aaatcgaagc
3351 ctagaaaaagt tgtacagaaa gcaacaagtc aaaaatatacg atcaacttca
3401 aaggttcaaa ttacatctta cagaccccaa aaaatgacag ttaacagaag

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3451 tcgactaaac agaaaccagc cagttcacc tggaaatgaag gagctttgat
3501 caatccatcc tagcttcatt ccccttgaa attgcagaca gagctctcat
3551 cctgctaaag ctggtggtt attcttaacc ctgcaatcaa taagcatgaa
3601 ctaacattgg acaccttcat cgccggattt ctcgaaaatc agtgagcgg
3651 ggatttacct gtgtgtgttag taacctctct ctttgatcat aaaatctgga
3701 aattccggca tcaactactg ccaccttct gcttaaggtg attttatcac
3751 caaggctgag cgtgattcct tgcgtcttgc tccgaatcct gatgtatcca
3801 ctgagcttccatctccttc ctctccagg cttatgttca ccaatgcgtc
3851 ctcgccgaac acactcttgg cgtacaagtt cgccagg aatccacact
3901 ctccatcaag tgcagacctg caaacccaa ataagaacac aaactccaaa
3951 gtcaacgatc aattctccgc cttttatgaa gaaaaggaaa cttctggta
4001 cttacggtgc cgtcagacac ttcatatgg tagacttgat gatatggtcc
4051 aggaattcct tctcggtctg aattgttgg ttaacagcaa cctgacagac
4101 agaaagatat cgcaaattta agatactggg atgacttaggc acagagaaat
4151 gaaatctaattctagaagta aaaccttatt ttcccattca aattctgccc
4201 acatagtccg gaacgcagca tccgagcaag aagcaggaga gatgtaatcc
4251 atgatatcga tgtggatatac gttgaggacg acaactgaac gttccatcac
4301 attgg

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_4 check: 8952 from: 1 to: 3501

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 134 Length: 21
Ratio: 6.381 Gaps: 0
Percent Similarity: 80.952 Percent Identity: 80.952

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 6777591_SEQ_4 December 15, 2006 17:08 ..

187 atgtcataaaattttactaaa 207
||||||| ||||| ||||| ||||
2977 atgtcagaaaatccttacgaaa 2997

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

1 gaattcggccc ttggtagatg tcttagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggc acgggattaa taggttccaa aaaccagccg
301 taaccttattt atattagggt actttaagct ggtgccctca gttttgttgg
351 tgtcttcgtt tttaaactta gttgtatTTT ttttcttagt tctgtccttc
401 tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata

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451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 6777591_SEQ_4

!NA_SEQUENCE 1.0
6777591_SEQ_4 Length: 3501 December 15, 2006 17:05 Type: N Check: 8952
..
1 tctagacatt tgacataaac cgaattcaaa gaacacaaca ttgactaaca
51 ccaaaaagaa atagagtagt gaaatttgga agataaaaaa atagaaacaa
101 actgattctt agaaagaaga gatgatttagg tgcttcagt tcggtctgtc
151 agggaaatcga gatgttcaact tatttacatt gtcgattcat ctcccaattg
201 tcctggttcc tttactgtcc gacgctttt tgaatccag ttaattccca
251 tcaagtcttc cttcagctgc gttagcactgc tagctccaac atggagcgtg
301 gagtctactc gttcatgggg catcgcaaag gtttgccttc atgttctgct
351 accagccagc gcccacgccc tcttggttgt gtggacaatt gcggtaagc
401 gcgcaagttg acatccata gtctcgacac ttcaccatat ggatgtttaa
451 aacgtataatc acgagtgcgta tctacatgtc ccatacacacc acatataaaag
501 caatagtttgcgaa gtagctttc atatttgcggg cggcatttgcgaaatcc
551 tctcgataat ttaatctttt tttctttca gctgattgtg tgcatccatt
601 cgggctcaga agcacatcaa agggatctct ccatacgatgttgcgt
651 gtcgtatgtat acgaagcagt cgatgaagtt tcctaatgtc cgagctacag
701 gctccgcggaa gaacccgcga ggttagatcgt atgctgtac ccaaaaatca
751 gtttgcgtatgtat gctccgcggaa cactagagac tcaccctaat gcatctcatg
801 tgtgatgaac agtttatcat ttgtgagtct aggggtcatt gtcgtatgttgcgt

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851 caatgcacat tgagcttatg atagaatttgc aataggaagc gttttccacc
901 cagatcacga atagctaccc cttttcggg cgccaaattt ccggcatcct
951 atcttccacc acaacttaaa gatgcgatcg gtaaggaact caccgaccac
1001 acacatcgaa taatcttcgg tgaccggttc ctgttgatca agtccctcaa
1051 tttcctcaac ctagtcttca atcgccgcta gcgttatccc ccgcataatgg
1101 actttcatag cgccggagcgt agccggagac gacgagcaag aaggatgagc
1151 ggcggcagat tgccggctaaa gaaacgagct tcctgccttg ctctatggag
1201 gcagatttct gagttgatgg tggatggattt gtgatgtgga cacttttaat
1251 ttaagttgat ttttagcac ttcattcacg taattaaata aataatttcc
1301 agtattttat atttatttcc ttacgttatac taatttttg aaagattaaa
1351 actttgatatacaggcaagatc atgacacgatc gaagttaaatgaaatgagact
1401 cctaacaagg taataacaaa gcagttcata aaccgaatga cttgtatctt
1451 tactaagctt gagatcatttgc aacatataat taaatacgat aatgaaagat
1501 aagaacttta atataaaaat cattcaaaac gagaactga taacaaaaac
1551 aaagcaaaacg gccaacaaaa taatagacgg tggaggatg atgcagagcc
1601 atccaccctt tttcccaagt ttccctactg ctatcttc tatgcataatc
1651 acaagacgcc cttgaaactt gttagtcatg cagagccctt actcgccagg
1701 tcacccgcacc acgtgttact ctatcacttc tcctccctt ctttaaaga
1751 accaccacgc caccccttc tcacaaacac tcataaaaaa accacctctt
1801 gcatttctcc caagttcaaa ttatgttaca gctaagcaag aactcaacaa
1851 caatggcgga tcgtacaaca cagccacacc aagtccaggt ccacacccag
1901 caccactatc ccaccggcgg ggcttcggc cgatgttgc gttatgttgc
1951 aggcggtcca catcaccacgc aaggatcagg cagcggccca tcagcttcca
2001 aggtgttagc agtcatgacc gcgcgtccca tcggcgggac cttccttgc
2051 ttggccggga taaccttggc tggacgtatg atcgggctgg cgatcaccac
2101 cccgatttt gtcatctgca gccctgttct agtcccgcc gctctgctca
2151 tcgggtttgc cgtgagcgcg tttctggcct cggggatggc cgggctgaca

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2201 gggctgacct cgctgtcgtg gtttgcgagg tatctgcgc aggctggca
2251 gggagttgga gtgggggtgc cgatagttt cgagcaggcg aagaggcgca
2301 tgcaggatgc tgctgggtat atggggcaga agaccaagga agttgggcag
2351 gagatccaga ggaagtctca ggatgtgaaa gcatcagaca aataaggtga
2401 taataagggg ttttgggttc gtgtgtaaac tggtaaaatg gaaattctgg
2451 gttttactgt acttttgcatt gtatgtgaaat gaatgagttc ttgttctctt
2501 ttgtctttta atcataaaagt aagaagcagc atttcatgtt ctgggttgaat
2551 attgtcaaga attcgcaaca aatttagcta aaccagttca atcttaccgg
2601 ttagacgact tcccagtaag aaacattcca ggtccatccc ggtataagag
2651 tctggacttc tgaaaccttt agaccttggaa tttggaaaaaa agatgaaacc
2701 tttagaataa attacaacga tggcagattt tacaaaactg gagtcgagat
2751 catgtaaatt agcccataac taagaaccgg cgatgacaac aattactagg
2801 aatatggttt ttgggctggt cggcggctag cggtgatgtat ttggaagaat
2851 cggggatcca gaatgtgaga accgaatcat cgacgaacat taccggcga
2901 ggagcccatt tcaagcaact ttggaactcc tataatggctg ttccagcagg
2951 ccacctgctc aagaaagaaaa gaagccatgt cagaatccct tacgaaatct
3001 aactggatgc tgatatgaat ccgccaggtt tgcggagttc tttacaggca
3051 ggatctataa agaagaaaca tggggcttat tggcattgtt gatgttccaa
3101 gcacgcagcg atctatctcc ggatcctaac aacaaaaata cggattctgt
3151 aagaaacaag cgcagaaaac ttctgcaacg aaaccactcg tataatggat
3201 tctgagttgg agaaagatga ccatactact gtatttggat gaaacttggat
3251 tggaaaccgaa attttggat gaaaagcgag tgatcgtata taaatccag
3301 attcagatta ggatatccta tgagagaagg tagagttacc tgatactaca
3351 tactgccccat caggggtaaa agttgcctcg atgggtgtt ttggagatgg
3401 ttccaggctta aatccacaac gctgaacaaa taaaagatg aatggatcaa
3451 tcttcaaccc ttacttctgc atttatgagg attggctcaa ggctctctag
3501 a

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_6 check: 6664 from: 1 to: 1676

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 169 Length: 34
Ratio: 4.971 Gaps: 0
Percent Similarity: 73.529 Percent Identity: 73.529

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 6777591_SEQ_6 December 15, 2006 17:08 ..

343 tttgttggtgtcttcgttttaaacttagttgtta 376
| ||| || |||| ||||||||| ||| ||| |
1617 tatgtatgtttcttgggttttaaaataaaatgga 1650

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

1 gaattcggccc ttggtagatg tcttagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taaccttattt atattagggt actttaagct ggtgccctca gttttgttgg
351 tgtcttcgtt tttaaactta gttgtatTTT ttttcttagt tctgtccttc
401 tagtgttata gagcataagg acaaaaattga gcaaaaaatg actaaggata

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451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 6777591_SEQ_6

!NA_SEQUENCE 1.0
6777591_SEQ_6 Length: 1676 December 15, 2006 17:06 Type: N Check: 6664
..
1 tccactatgt aggtcatatc catcattta attttggc accattcaat
51 tccatcttgc cttagggat gtgaatatga acggccaagg taagagaata
101 aaaataatcc aaattaaagc aagagaggcc aagtaagata atccaaatgt
151 acacttgtca tcgcccgaat tagtaaaata cgccgcata tgcatttcca
201 cacattatta aaataccgta tatgtattgg ctgcatttgc atgaataata
251 ctacgtgtaa gcccaaaaga acccacgtgt agcccattgca aagttaacac
301 tcacgacccc attcctcagt ctccactata taaaccacc atccccaaatc
351 ttaccaaacc caccacacga ctcacaactc gactctcaca ccttaaagaa
401 ccaatcacca ccaaaaaatg gcaaagctga tgagcctagc agccgtagca
451 acgcagttcc tcttcctgat cgtggggac gcatccgtcc gaaccacagt
501 gattatcgac gaggagacca accaaggccg cggtggaggc aaggtggcag
551 ggacagcagc agtctgcgag cagcagatcc agcagcgaga cttcctgagg
601 agctgccagc agttcatgtg ggagaaagtc cagagggcg gccacagcca
651 ctattacaac cagggccgtg gaggaggcga acagagccag tacttcgaac
701 agctgtttgt gacgaccta agcaattgcg caccgcgtg caccatgcc
751 ggggacttga agcgtgccat cggccaaatg aggcaggaaa tccagcagca
801 gggacagcagc cagggacagc agcaggaagt tcagaggtgg atccagcaag

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851 ctaaacaat cgctaaggac ctccccggac agtgccgcac ccagcctagc
901 caatgccagt tccagggcca gcagcaatct gcatggttt gaaggggtga
951 tcgattatga gatcgtacaa agacactgct aggtgttaag gatggataat
1001 aataataata atgagatgaa tgtgtttaa gttagtgtaa cagctgtaat
1051 aaagagagag agagagagag agagagagag agagagagag agagagagag
1101 agaggctgat gaaatgttat gtatgttct tggttttaa aataaatgaa
1151 agcacatgct cgtgtggttc tatcgaatta ttcggcggtt cctgtggaa
1201 aaagtccaga agggcgccg cagctactac tacaaccaag gccgtggagg
1251 agggcaacag agccagcact tcgatagctg ctgcgatgat cttaagcaat
1301 tgaggagcga gtgcacatgc agggactgg agcgtcaat cggccagatg
1351 aggcaggaca tccagcagca gggacagcag caggaagttg agaggtggc
1401 ccatcaatct aaacaagtcg cttagggacct tccgggacag tgcggcaccc
1451 agcctagccg atgccagctc caggggcagc agcagtctgc atggtttga
1501 agtggtgatc gatgagatcg tataaagaca ctgctaggtg ttaaggatgg
1551 gataataaga tgtgtttaa gtcattaacc gtaataaaaa gagagagagg
1601 ctgatggaat gttatgtatg tatgtttctt ggttttaaa attaaatgga
1651 aagcacatgc tcgtgtgggt tctatc

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_8 check: 1234 from: 1 to: 4999

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 445 Length: 379
Ratio: 1.233 Gaps: 7
Percent Similarity: 61.224 Percent Identity: 39.650

Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 6777591_SEQ_8 December 15, 2006 17:09 ..

226 catgtcataactgaacttgtgagaaaaacgccagttatttatggtacggg 275
||: : :|: | :|| |||:| | | | |: ||||:|
4543 canaancnangtanattaaaaganatggaaattaantaatggna.... 4588

276 attaatagttccaaaaaccagccgtAACCTATTAA....tattaggg 320
||:|:||| :| | | |: |:|| : :| | | |||:|
4589 atnannaggaggattgnaacggcngancgnangaanagtttanngg 4638

321 actttaagctgtgcctcagtttgttggtgtcttcgttttaactta 370
| | |||| | | | :|: | :| :| || : |||
4639 tttaaatactgggg.....gagtnagnagccngccnctggttccngtga 4682

371 gttgtatTTTTCTTAGTTCTGTCCCTCTAGTGTATAGAGCATAAGG 420
| :| | :||| :| | | :|:|| :||| | |||
4683 gangaaaccaagnncggg...aggnTnCannnnnagggagaaaaagg 4729

421 acaaaattgagcaa.....aaaatgactaaggataaaaatgaggat 463
|::| | ||:|:|:| | | ||| :| | :| | ||:|| |
4730 anncaTTnannnangcngaggacatgaancggtaCngagCTGNGTTCA 4779

464 cagaaaggcagcagctaaaaaccttt.....tatattatggatt 507
:::|:|| |::: :| | :: : :| | | :|||
4780 nnnancgg.....cgnnnnggnagtcccnnngggaccnggntgggtan 4824

508 ggacaccagtctataaaaagtatactccaaggcacatttgaattggatt 557
|| |: | | | :|:|: :|: | :|| | :||| | |||
4825 ggaaanggaacatnggtngnangganaanaccnTTTACNATTGCTTT 4874

558 gcattgtcagtcaaggccagtcaaggggac 586

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||| ::: : :|||: :|: || :||
4875 gcaggnngtntngcncntncggtnac 4903

Input Sequence: 1587_SEQ_1

!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..
1 gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taaccttattt atattagggt actttaagct ggtgcctca gttttgttgg
351 tgtcttcgtt tttaaactta gttgtatttt ttttcttagt tctgtccttc
401 tagtgttata gacgataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggcagtc当地 ggggaccatg

Input Sequence: 6777591_SEQ_8

!NA_SEQUENCE 1.0
6777591_SEQ_8 Length: 4999 December 15, 2006 17:07 Type: N Check: 1234 ..
1 ctcaagcata cggacaaggg taaataacat agtcaccaga acataataaa
51 caaaaagtgc agaagcaaga taaaaaaatt agctatggac attcaggttc
101 atattggaaa catcatttac ctgtcttgt gaccatcctt cctcctgctc

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151 tagttgagag gccttggac taacgagagg tcagttggga tagcagatcc
201 ttatcctgga ctgccttc tggtgttca gagtcctcgt gccgccgtct
251 acatctatct ccattaggc tgaagatgac tcttcacacc aacgacgtt
301 aaggtctcta tcctactcct agcttgcaat acctggcttg caatacctgg
351 agcatcgtgc acgatgattg gatactgtgg aggaggagtg tttgctgatt
401 tagagctccc gggtgggtga tttgacttcg atttcagttt aggcttgttg
451 aaattttca ggttccattt gtaagcctt agagcttgag cttccttcca
501 tgttaatgcc ttgatcgaat tctcctagag aaaaggaaag tcgatctctg
551 agtattgaaa tcgaagtgc cattttttt caacgtgtcc aatcaatcca
601 caaacaaagc agaagacagg taatcttca tacttatact gacaagtaat
651 agtcttaccg tcatgcataa taacgtctcg ttccttcaag aggggttttc
701 cgacatccat aacgaccgaa agcctcatga aagcattagg gaagaacttt
751 tggttcttct tgtcatggcc tttataggtg tcagccgagc tcgccaattc
801 ccgtccgact ggctccgaa aatattcgaa cgccaagtt tggacttgca
851 accataactc cacggatttgc agcaggacct attgtgaaga ctcatctcat
901 ggagcttcag aatgtggttg tcagcaaacc aatgaccgaa atccatcaca
951 tgacggacgt ccagtgggtg agcgaaacga aacaggaagc gcctatctt
1001 cagagtcgtg agctccacac cgattccgg caactacgtg ttggcagggc
1051 ttgcgcgtat tagagatatg ttgaggcaag acccatctgt gccactcgta
1101 caattacgag agttttttt ttgtgattt tcctaagtt ctcgttgatg
1151 gtgagctcat attctacatc gtatggtctc tcaacgtcgt ttcctgtcat
1201 ctgatatccc gtcatttgca tccacgtcg ccgcctcccg tgccaagttc
1251 ctaggtgtca tgcacgccaa attgggtggt gtgcgggctg ccctgtgctt
1301 cttaccgatg ggtggagggtt gagttgggg gtctccgcgg cgatggtagt
1351 ggggtgacgg tttgggtgtgg gttgacggca ttgatcaatt tacttcttgc
1401 ttcaaattct ttggcagaaa acaattcatt agattagaac tggaaaccag
1451 agtgatgaga cggattaagt cagattccaa cagagttaca tctcttaaga

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1501 aataatgtaa cccctttaga ctttatataat ttgcaattaa aaaaataatt
1551 taacttttag actttatata tagtttaat aactaagttt aaccactcta
1601 ttatttatata cgaaaactatt tggatgtctc ccctctaaat aaacttggt
1651 ttgtgtttac agaacctata atcaaataat caataactcaa ctgaagttt
1701 tgcagttaat tgaaggatt aacggccaaa atgcactagt attatcaacc
1751 gaatagattc acactagatg gccatttcca tcaatatcat cgccgttctt
1801 cttctgtcca catatcccct ctgaaacttg agagacacct gcacttcatt
1851 gtccttatta cgtgttacaa aatgaaaccc atgcatccat gcaaactgaa
1901 gaatggcgca agaacccttc ccctccattt cttatgtggc gaccatccat
1951 ttcaccatct cccgtataaa aacacccccc tcacttcacc tagaacatca
2001 tcactacttg cttatccatc caaaagatac ccaccatggc tagatcatca
2051 agcccttgc ttctctcact ctgcattttc gccattctct tccactcttc
2101 tctggtagg cagcaattcc agcaggggaa cgagtgccag atcgacagga
2151 tcgacgcattc cgagccggac aaaaccatcc aggcagaagc tggcaccatc
2201 gaggtatggg accagaaccg ccagcaattc cagtgcgctg gtgtgccgt
2251 tgtaaggcgc accattgagc ccaaaggcttct tctcttgcc ttctacagca
2301 acacccctca gctcatctac atcggtcaag gtataaatta aatcagttca
2351 tacaatgata accaccactt cgaatgtatt tatcaaataat caatgatcga
2401 tgcacctgta tgtgttgtgt atattcaggt aggggagttt caggaatcat
2451 gttccakga tgtccagaga cattcgagga atcccagcag caaggacaac
2501 agggccaaca gggtagttcc caagaccagc accagaagat ccggccgttc
2551 cgtgaaggtg acgtcattgc cgtccctgcc ggttagccc actggtccta
2601 caacgatggc aacgaaccag tcatggccat tggtgtccat gacacttcca
2651 gccacctcaa ccaactggac aacaacccca gggtatataa gcattgccgt
2701 agttgctaattaaattgcaca caattggAAC tctatTTCA gtatctaata
2751 acttttcct ttttggcag aacttctact tggcaggaaa cccgagagac
2801 gagttcgaac aatcgagca aggaggcagg ctgagccgtg gggagagtgaa

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2851 aggtggacga ggacgcaggg aacctttca acctgcaaca acctttctt
2901 gcggaatcga ctccaagctc atcgcgagg cgttcaatgt cgacgagaac
2951 gtggcaagga ggctacagag cgagaacgac aacagaggcc agatcgtccg
3001 agtcgaaggc gagctcgaca tcgtcagacc tccgaccagt atccaggagg
3051 agtcacagga gcagggaggt cgtgggttg gccgctacta ctccaatgga
3101 gtggaggaga cttctgctc catgagacta attgagaaca tcggcgatcc
3151 ttctcgggca gacatttca ctccagaagc cggccgcgtt agatccctca
3201 acagccacaa cttcccgtc ctgcaatgga tccagcttag cgccgagaga
3251 ggcgttctct acaatgtata gatctcactc acgcaccaac tctaaattga
3301 atccctaatt atttaattca ccgatatctg accgaccggt ttgaatttg
3351 taggaagcga tcaggctgcc gcactggaac atcaacgcac acagcatagt
3401 gtacgcgatc agaggacaag ccagagtcca gatcgtgaac gaggaaggaa
3451 attcgggttt cgatggagtg ctgcaggaag gacaggtgg gacggtgccg
3501 cagaacttcg cgggtttaaa gagatcccag agcgagaggt ttgagtgggt
3551 ggcgttcaag accaacgaca acgcgatggt gaactcgcta gccgggagga
3601 catcggcagt aaggcgatc cccgcggatg tactgctaa cgcctggagg
3651 gtgtcgccgg aggaggcgag gagggtgaag ttcaacaggc aggagactca
3701 ctggcttagc accaggggcc agtccaggtc gcccggagg ttgaatgtcg
3751 tcaaggaggt gatcaacttg ctatgtaaa atgtgacggt gaaataataa
3801 cggtaaaata tatgtataaa taataataat aaagccacaa agtgagaatg
3851 agggaaaggg gaaatgtgt atgagccagt agccgggtgg gctaattttg
3901 tattgtattt tcaataaaatc atgaattttg tggttttat gtgtttttt
3951 aaatcatgaa ttttaaattt tataaaataa tctccaatcg gaagaacaac
4001 attccatatc catggatgtt tctttaccca aatctagttc ttgagaggat
4051 gaagcatcac cgaacagttc tgcaactatc cctcaaaagc tttaaaatga
4101 acaacaagga acagagcaac gttccaaaga tcccaaacga aacatattat
4151 ctatactaactatattat taattactac tgcccgaaat cacaatccct

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4201 gaatgattcc tattaactac aagccttgtt ggcggcggag aagtgatcg
4251 cgccggcgaga agcagcggac tcggagacga ggccttggat gagcagagtc
4301 tttacctgcc agggcgtgaa ggggaagagc ggccttctgg agtaggagtt
4351 cagcaagcgg cggttccttg gcggagtaag cggacgtaag ggtggntg
4401 gacgtcncgt tttcnggagg cgnattcatg aagggttaaa gtcanaatctg
4451 tagctctcga gtgctcaggg agccnaaaga cgttggaaa ccgtcgn
4501 ttggggcatc agtcngcgg gcacgcttcc ctccctgctgc tccanaanc
4551 angtanattt aaaaganatg gaaattnaat taatgnaat nannaggagg
4601 attgnaacgg tcngancgn angaanagtt tttanngtt taaatactgg
4651 gggagtngna gccngccnct ggttccngtg tagangaaac caagnnccgg
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4751 gacatgaanc ggtacngagc tgnggttcan nnancggcgn nnggnagtc
4801 cnngggacn ggntgggttn anaaggaaan ggaacatng gtngnangga
4851 naanaccnntt ttacnattgc ctgcaggn nngtnnggc ncncnccgg
4901 nacatnccgc tgcatggct ttggggngcc nanagnagc cncangggna
4951 nnccnccncc ttgtncangn cgctnaagtt cnattgtana tggncgtt